In the Claims:

1. (Original) A method of diagnosing a subject with multiple sclerosis, the method comprising determining a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between said level of expression of said gene in said sample obtained from said subject and a normal expression level of said gene is an indication that the subject is afflicted with multiple sclerosis.

2. (Original) The method of claim 1, wherein said normal expression level of said at least one gene is determined by measuring said level of expression of said gene in at least one control sample obtained from at least one healthy individual.

3. (Original) The method of claim 2, wherein said sample includes peripheral blood mononuclear cells.

4. (Original) The method of claim 1, wherein said substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

5. (Original) The method of claim 1, wherein said level of expression of said at least one gene is determined by quantifying a level of a protein product thereof in said sample.

6. (Original) The method of claim 5, wherein quantifying a level of said protein is effected using a reagent which specifically binds with said protein.

7. (Original) The method of claim 6, wherein said reagent comprises an antibody or fragments thereof.

8. (Original) The method of claim 1, wherein said at least one gene is selected from the genes listed in Table I.

9. (Original) The method of claim 1, wherein said at least one gene is selected from the genes listed in Table II.

10. (Original) The method of claim 1, wherein said at least one gene is selected from the genes listed in Table III.

11. (Original) The method of claim 1, wherein said at least one gene is selected from the genes listed in Table IV.

12. (Original) The method of claim 1, wherein said at least one gene is selected from the genes listed in Table V.

13. (Original) The method of claim 1, wherein the level of expression of said at least one gene in said sample is determined by detecting the presence in said sample of a transcribed polynucleotide or portion thereof.

14. (Original) The method of claim 13, wherein said transcribed polynucleotide is mRNA.

15. (Original) The method of claim 13, wherein said transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with said transcribed polynucleotide or portion thereof.

16. (Original) The method of claim 1, wherein said sample from a subject is T cells, and said at least one gene is selected from the genes listed in Table IV and whereas said normal expression of said gene is T-cell expression.

17. (Original) The method of claim 16, wherein said substantial difference is at least a 1.5 fold change.

18. (Original) The method of claim 1, wherein said at least one gene comprises at least 10 genes each independently selected from the group consisting of the genes listed in Tables I-V.

19. (Original) The method of claim 1, wherein said at least one gene comprises at least 50 genes each independently selected from the group consisting of the genes listed in Tables I-V.

20. (Original) The method of claim 1, wherein said at least one gene comprises at least 100 genes each independently selected from the group consisting of the genes listed in Tables I-V.

21. (Original) The method of claim 1, wherein said at least one gene comprises at least 250 genes each independently selected from the group consisting of the genes listed in Tables I-V.

22. (Original) The method of claim 1, wherein said at least one gene comprises at least 500 genes each independently selected from the group consisting of the genes listed in Tables I-V.

23. (Original) The method of claim 1, wherein said at least one gene comprises at least 750 genes each independently selected from the group consisting of the genes listed in Tables I-V.

24. (Original) The method of claim 1, wherein said at least one gene comprises at least 1000 genes each independently selected from the group consisting of the genes listed in Tables I-V.

25. (Original) The method of claim 1, wherein said at least one gene comprises at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V.

26. (Original) A method of diagnosing a subject with multiple sclerosis, the method comprising the step of determining a level of expression of each of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between expression levels of said genes in said sample obtained from said subject and normal expression levels of said genes is an indication that the subject is afflicted with multiple sclerosis.

27. (Original) The method of claim 26, wherein said normal expression levels of said genes is determined by measuring said level of expression of said genes in at least one control sample obtained from at least one healthy individual.

28. (Currently Amended) The method of claim ~~29~~ 26, wherein said sample includes peripheral blood mononuclear cells.

29. (Original) The method of claim 26, wherein said substantial difference is a difference statistically significant at a confidence level of p= 0.05 as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

30. (Original) The method of claim 26, wherein said level of expression of said genes is determined by quantifying a level of a protein product thereof in said sample.

31. (Original) The method of claim 30, wherein quantifying a level of said protein is effected using a reagent which specifically binds with said protein.

32. (Original) The method of claim 31, wherein said reagent comprises an antibody or fragments thereof.

33. (Original) The method of claim 26, wherein the level of expression of said genes in said sample is determined by detecting the presence in said sample of a transcribed polynucleotide or portion thereof.

34. (Original) The method of claim 33, wherein said transcribed polynucleotide is mRNA.

35. (Original) The method of claim 34, wherein said transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with said transcribed polynucleotide or portion thereof.

36. (Original) A method of monitoring a state of multiple sclerosis in a subject, the method comprising monitoring a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V over a predetermined time period, wherein substantial difference between the levels of expression of said at least one gene over said predetermined time period indicates a change in a state of the multiple sclerosis in the subject.

37. (Original) The method of claim 36, wherein monitoring said level of expression of at least one gene over said predetermined time period is effected by periodically obtaining a sample from the individual and determining said level of expression of said at least one gene in said sample.

38. (Original) The method of claim 37, wherein said sample includes peripheral blood mononuclear cells.

39. (Original) The method of claim 36, wherein said substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

40. (Original) The method of claim 36, wherein said level of expression of said at least one gene is determined by quantifying a level of a protein product thereof in said sample.

41. (Original) The method of claim 36, wherein quantifying a level of said protein is effected using a reagent which specifically binds with said protein.

42. (Original) The method of claim 41, wherein said reagent comprises an antibody or fragments thereof.

43. (Original) The method of claim 36, wherein said at least one gene is selected from the genes listed in Table I.

44. (Original) The method of claim 36, wherein said at least one gene is selected from the genes listed in Table II.

45. (Original) The method of claim 36, wherein said at least one gene is selected from the genes listed in Table III.

46. (Original) The method of claim 36, wherein said at least one gene is selected from the genes listed in Table IV.

47. (Original) The method of claim 36, wherein said at least one gene is selected from the genes listed in Table V.

48. (Original) The method of claim 36, wherein the level of expression of said at least one gene in said sample is determined by detecting the presence in said sample of a transcribed polynucleotide or portion thereof.

49. (Original) The method of claim 48, wherein said transcribed polynucleotide is mRNA.

50. (Original) The method of claim 48, wherein said transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with said transcribed polynucleotide or portion thereof.

51. (Original) The method of claim 36, wherein said sample from a subject is T cells, and said at least one gene is selected from the genes listed in Table IV and whereas said normal expression of said gene is T-cell expression.

52. (Original) The method of claim 51, wherein said substantial difference is at least a 1.5 fold change.

53. (Original) The method of claim 36, wherein said at least one gene comprises at least 10 genes each independently selected from the group consisting of the genes listed in Tables I-V.

54. (Original) The method of claim 36, wherein said at least one gene comprises at least 50 genes each independently selected from the group consisting of the genes listed in Tables I-V.

55. (Original) The method of claim 36, wherein said at least one gene comprises at least 100 genes each independently selected from the group consisting of the genes listed in Tables I-V.

56. (Original) The method of claim 36, wherein said at least one gene comprises at least 250 genes each independently selected from the group consisting of the genes listed in Tables I-V.

57. (Original) The method of claim 36, wherein said at least one gene comprises at least 500 genes each independently selected from the group consisting of the genes listed in Tables I-V.

58. (Original) The method of claim 36, wherein said at least one gene comprises at least 750 genes each independently selected from the group consisting of the genes listed in Tables I-V.

59. (Original) The method of claim 36, wherein said at least one gene comprises at least 1000 genes each independently selected from the group consisting of the genes listed in Tables I-V.

60. (Original) The method of claim 36, wherein said at least one gene comprises at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V.

61. (Original) A method of assessing the efficacy of a treatment regimen on multiple sclerosis in a subject, the method comprising determining a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V in samples obtained from the subject prior to, and following exposure to the treatment regimen, wherein a substantial difference in the expression level of said

at least one gene between said samples is an indication that the treatment regimen is efficacious in treating multiple sclerosis in said subject.

62. (Original) The method of claim 61, wherein said treatment regimen is administering at least one test compound for inhibiting multiple sclerosis.

63. (Original) The method of claim 61, wherein said treatment regimen is an environmental condition.

64. (Original) The method of claim 61, wherein said samples include peripheral blood mononuclear cells.

65. (Original) The method of claim 61, wherein said substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

66. (Original) The method of claim 61, wherein said level of expression of said at least one gene is determined by quantifying a level of a protein product thereof in said sample.

67. (Original) The method of claim 66, wherein quantifying a level of said protein is effected using a reagent which specifically binds with said protein.

68. (Original) The method of claim 67, wherein said reagent comprises an antibody or fragments thereof.

69. (Original) The method of claim 61, wherein said at least one gene is selected from the genes listed in Table I.

70. (Original) The method of claim 61, wherein said at least one gene is selected from the genes listed in Table II.

71. (Original) The method of claim 61, wherein said at least one gene is selected from the genes listed in Table III.

72. (Original) The method of claim 61, wherein said at least one gene is selected from the genes listed in Table IV.

73. (Original) The method of claim 61, wherein said at least one gene is selected from the genes listed in Table V.

74. (Original) The method of claim 61, wherein the level of expression of said at least one gene in said samples is determined by detecting the presence in said samples of a transcribed polynucleotide or portion thereof.

75. (Original) The method of claim 74, wherein said transcribed polynucleotide is mRNA.

76. (Original) The method of claim 74, wherein said transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with said transcribed polynucleotide or portion thereof.

77. (Original) The method of claim 61, wherein said at least one gene comprises at least 10 genes each independently selected from the group consisting of the genes listed in Tables I-V.

78. (Original) The method of claim 61, wherein said at least one gene comprises at least 50 genes each independently selected from the group consisting of the genes listed in Tables I-V.

79. (Original) The method of claim 61, wherein said at least one gene comprises at least 100 genes each independently selected from the group consisting of the genes listed in Tables I-V.

80. (Original) The method of claim 61, wherein said at least one gene comprises at least 250 genes each independently selected from the group consisting of the genes listed in Tables I-V.

81. (Original) The method of claim 61, wherein said at least one gene comprises at least 500 genes each independently selected from the group consisting of the genes listed in Tables I-V.

82. (Original) The method of claim 61, wherein said at least one gene comprises at least 750 genes each independently selected from the group consisting of the genes listed in Tables I-V.

83. (Original) The method of claim 61, wherein said at least one gene comprises at least 1000 genes each independently selected from the group consisting of the genes listed in Tables I-V.

84. (Original) The method of claim 61, wherein said at least one gene comprises at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V.

85. (Original) A kit for diagnosing multiple sclerosis in a subject, the kit comprising components suitable for determining expression levels of at least one gene selected from the group of genes listed in Tables I-V.

86. (Original) The kit of claim 85, wherein said reagents include at least one polynucleotide sequence selected capable of specifically hybridizing with an transcription product of said at least one gene and reagents for detecting and optionally quantifying a complex formed from said at least one polynucleotide sequence and said transcription product.

87. (Original) The kit of claim 85, wherein said reagents include at least one antibody selected capable of specifically binding a polypeptide product of said at least one gene and reagents for detecting and optionally quantifying a complex formed from said at least one antibody and said polypeptide product.

88. (Original) The kit of claim 85, wherein said at least one gene is selected from the genes listed in Table I.

89. (Original) The kit of claim 85, wherein said at least one gene is selected from the genes listed in Table II.

90. (Original) The kit of claim 85, wherein said at least one gene is selected from the genes listed in Table III.

91. (Original) The method of claim 88, wherein said at least one gene is selected from the genes listed in Table IV.

92. (Original) The method of claim 85, wherein said at least one gene is selected from the genes listed in Table V.

93. (Original) The kit of claim 85, wherein the kit further comprises packaging material identifying the kit as useful from diagnosing MS.

94. (Original) A polynucleotide array comprising at least 10 and no more than 1500 polynucleotide sequences, wherein each of said sequences is selected capable of hybridizing with a transcription product of a polynucleotide sequence of a gene selected from the group of genes listed in Tables I-V.

95. (Original) The polynucleotide array of claim 94, wherein said array is selected having polynucleotide sequences capable of diagnosing subjects suspected of suffering from multiple sclerosis.

96. (Original) The polynucleotide array of claim 94, wherein said array is selected having polynucleotide sequences capable of diagnosing subjects suspected of suffering from probable multiple sclerosis.

97. (Original) The polynucleotide array of claim 94, wherein said array is selected capable of diagnosing subjects suspected of suffering from primary progressive multiple sclerosis.

98. (Original) The polynucleotide array of claim 94, wherein said array is selected capable of diagnosing subjects suspected of suffering from relapsing multiple sclerosis.

99. (Original) The polynucleotide array of claim 94, wherein said gene is selected from the genes listed in Table I.

100. (Original) The polynucleotide array of claim 94, wherein said gene is selected from the genes listed in Table II.

101. (Original) The polynucleotide array of claim 94, wherein said gene is selected from the genes listed in Table III.

102. (Original) The polynucleotide array of claim 94, wherein said gene is selected from the genes listed in Table IV.

103. (Original) The polynucleotide array of claim 94, wherein said gene is selected from the genes listed in Table V.

104. (Original) An array comprising at least 10 and no more than 1500 antibodies or antibody fragments each capable of specifically binding a protein product of a gene selected from the group of genes listed in Tables I-V.

105. (Original) The array of claim 104, wherein said array is selected having antibodies or antibody fragments capable of diagnosing subjects suspected of suffering from multiple sclerosis.

106. (Original) The array of claim 104, wherein said array is selected having antibodies or antibody fragments capable of diagnosing subjects suspected of suffering from probable multiple sclerosis.

107. (Original) The array of claim 104, wherein said array is selected capable of diagnosing subjects suspected of suffering from primary progressive multiple sclerosis.

108. (Original) The array of claim 104, wherein said array is selected capable of diagnosing subjects suspected of suffering from relapsing multiple sclerosis.

109. (Original) The array of claim 104, wherein said gene is selected from the genes listed in Table I.

110. (Original) The array of claim 104, wherein said gene is selected from the genes listed in Table II.

111. (Original) The array of claim 104, wherein said gene is selected from the genes listed in Table III.

112. (Original) The array of claim 104, wherein said gene is selected from the genes listed in Table IV.

113. (Original) The array of claim 104, wherein said gene is selected from the genes listed in Table V.